USPTO Form 1449 Patent and Trademark OS TABLE SUPPLEMENTAL INFORMATION DISCLOSURE				Attorney Docket No. 8039/1090		Serial No. 09/710,444		
SUPPLEN STATEM		L INFORMATION I	DISCLOSURE	Applicant(s):. Rie				
				Filing Date: Nove			Group: 525	3
U.S. PAT	ENT DO	DCUMENTS						
Examiner Initial		Patent No.	Date	Name	Class	Subclass	Filing I (if appro	
FOREIGN	I PATE	NT DOCUMENTS					,	
Examiner Initial		Document No.	Publication Date	Country	Class	Subclass	Translation	
102				<u>'</u>	_	•	YES	NO
MD	1.	WO92/01047	January 23, 1992	PCT	C12N	15/00		
405	2.	WO90/14430	November 29, 1990	PCT	C12P	19/34		<u> </u>
405	3.	WO92/20791	November 26, 1992	PCT	C12N	15/00		
ZOA	4.	WO90/05144	May 17, 1990	PCT	C07K	13/00		
FAZ	5.	WO93/11236	June 10, 1993	PCT	C12N	15/13		<u> </u>
OTHER I	OCUM	 IENTS (including Au	thor, Title, Date, Pertiner	nt Pages, etc.)				<u> </u>
			Λ		 ,	· · · · · · · · · · · · · · · · · · ·		
EXAMIN	ER	Fralk/ (P	Looka		DATE C	ONSIDERED) S	
EXAMINER:	nitial if refer	ence considered, whether or not cita	tion is in conformance with MPER 609. D	Traw line through citation if no	t in conformance a	nd not considered	. Include copy of the	ais form wi
		ovided at the time of this submission						

JIIL 2 7 2000 F.

RECEIVED

	E				TE	CH CENTE	R 1600/2	900
USPTO Form 1449 U.S. Department of Commerce Pauent and Trademark Office HADE			Attorney Docket No.		Serial No.			
INFORMATION DISCLOSURE STATEMENT			8654/1090		09/710,444			
			Applicant(s):. Riechmann, et al					
				Filing Date: Novembe	r 10, 2000		Group:	
U.S. PAT	ENT D	OCUMENTS						
Examiner Initial		Patent No.	Date	Name	Class	Subclass	Filing (if appr	
ronnya)					<u></u>	·	<u> </u>	
FOREIGN Examiner	FOREIGN PATENT DOCUMENTS Examiner Document No. Date Country Class Subclass				Trans	Translation		
Initial		Document 140.	Juic	Country	Class	Succiass	YES	NO
			·				123	
OTHER D	OCUM	ENTS (including Aut	hor, Title, Date, Per	tinent Pages, etc.)	<u> </u>	L		
1	Rubingh, D.N. (1997). Protein engineering from a bioindustrial point of view. Current Opinion in Biotechnology. 8, 417-422.						in	
2		Fersht, A.R. (1993). Protein folding and stability: the pathway of folding of barnase. FEBS Letters. 325, 5-16.						
3	AS	Zhao, H., et al. (1998). Molecular evolution by staggered extension process (StEP) in vitro recombination. Nature Biotechnology. 16, 258-261.						
4	MS	Patten, P.A., R.J. Howard, and W.P.C. Stemmer. (1997). Applications of DNA shuffling to pharmaceuticals and vaccines. <i>Current Opinion in Biotechnology</i> . 8, 724-733.						
5	ND	Sauer, R.T. (1996). Protein folding from a combinatorial perspective. Folding & Design. 1, R27-R30.						
6	MS	Dahiyat, B.I., C.A. Sarisky, and S.L. Mayo. (1997). Dc Novo Protein Design: Towards Fully Automated Sequence Selection. <i>Journal of Molecular Biology</i> . 273, 789-796.						
7	B	Riddle, D.S., et al. (1997). Functional rapidly folding proteins from simplified amino acid sequences. Nature Structural Biology. 4(10), 805-809.						
8	B	Hoogenboom, H.R. and G. Winter. (1992). By-passing Immunisation. Human Antibodies from Synthetic Repertoires of Germline VH Gene Segments Rearranged in Vitro. Journal of Molecular Biology. 227, 381-388.						
9	B	Winter, G., et al. (1994). Making Antibodies by Phage Display Technology. Annual Review of Immunology. 12, 433-455.						
10	MS	Braisted, A.C. and J.A. Wells. (1996). Minimizing a binding domain from protein A. Proc. Natl. Acad. Sci. USA. 93, 5688-5692.						
11	MS	Gu, H., et al. (1995). A phage display system for studying the sequence determinants of protein folding. <i>Protein Science</i> . 4, 1108-1117.						
12	W	Hubbard, S.J., F. Eisenmenger, and J.M. Thornton. (1994). Modeling studies of the change in conformation required for cleavage of limited proteolytic sites. <i>Protein Science</i> . 3, 757-768.						
13	M	Fontana, A., et al. (1997). Probing the partly folded states of proteins by limited proteolysis. Folding & Design. 2, R17-R26.						

RECEIVED
JUL 3 Page 2 of 3

<u>E</u>		TECH CENTER 1600/2000
142	Mes	Kamtekar, S., et al. (1993). Protein Design by Binary Patterning of Polar and Nonpolar Amino Acids.
THE TRA		Science. 262, 1680-1685.
15	220	Davidson, A.R. and R.T. Sauer. (1994). Folded proteins occur frequently in libraries of random amino
	HD)	acid sequences. Proc. Natl. Acad. Sci. USA. 91, 2146-2150.
16	20	Davidson, A.R., K.J. Lumb, and R.T. Sauer. (1995). Cooperatively folded proteins in random
	160	sequence libraries. Nature Structural Biology. 2(10), 856-864.
17		Matthews, D.J. and J.A. Wells. (1993). Substrate Phage: Selection of Protease Substrates by
''	MM	Monovalent Phage Display. Science. 260, 1113-1117.
18	That A	Riechmann, L. and P. Holliger. (1997). The C-Terminal Domain of TolA Is the Coreceptor for
10	DAY!	Filamentous Phage Infection of E. coli. Cell. 90, 351-360.
19	1415	Thankenous Thage infection of E. con. Cen. 70, 331-300.
19	I Karl	Smith C.D. (1995) Filamentaus Fusion Phones Novel Functions Vestors That Display Claused
	IMM VI	Smith, G.P. (1985). Filamentous Fusion Phage: Novel Expression Vectors That Display Cloned
	1,6	Antigens on the Virion Surface. Science. 228, 1315-1317.
20	Kara	Krebber, C., et al. (1997). Selectively-infective Phage (SIP): A Mechanistic Dissection of a Novel in
	INK)	vivo Selection for Protein-ligand Interactions. Journal of Molecular Biology. 268, 607-618.
21	M	Stengele, I., et al. (1990). Dissection of Functional Domains in Phage fd Adsorption Protein.
	MA	Discrimination between Attachment and Penetration. Journal of Molecular Biology. 212, 143-149.
22		Gray, C.W., R.S. Brown, and D.A. Marvin. (1981). Adsorption complex of Filamentous fd virus. Journal
	MO	of Molecular Biology. 146, 621-627.
23	4 2	Hoogenboom, H.R., et al. (1991). Multi-subunit proteins on the surface of filamentous phage:
	VVM	methodologies for displaying antibody (Fab) heavy and light chains. Nucleic Acids Research. 19,
	11154	4133-4137.
24	W0	Bass, S., R. Greene, and J.A. Wells. (1990). Hormone Phage: An Enrichment Method for Variant
	14/60	Proteins With Altered Binding Properties. Proteins. 8, 309-314.
25	200	Nissim, A., et al. (1994). Antibody fragments from a "single pot" phage display library as
		immunochemical reagents. The EMBO Journal. 13, 692-698.
26	200	Marzari, R., et al. (1997). Extending filamentous phage host range by the grafting of a heterologous
	$ \mathcal{U}\mathcal{M} $	receptor binding domain. Gene. 185, 27-33.
27	000	Mossakowska, D.E., K. Nyberg, and A.R. Fersht. (1989). Kinetic Characterisation of the
	HVXX I	Recombinant Ribonuclease from Bacillus amyloliquefaciens (Barnase) and Investigation of Key
	12	Residues in Catalysis by Site-Directed Mutagenesis. Biochemistry. 28, 3843-3850.
28	220	Meiering, E.M., L. Serrano, and A.R. Fersht. (1992). Effect of Active Site Residues in Barnase on
	MODI	Activity and Stability. Journal of Molecular Biology. 225, 585-589.
29	100	Serrano, L., et al. (1992). The Folding of an Enzyme. II Substructure of Barnase and the Contribution
	MYD	of Different Interactions to Protein Stability. Journal of Molecular Biology. 224, 783-804.
30	12	McKnight, C.J., P.T. Matsudaira, and P.S. Kim. (1997). NMR structure of the 35-residue villin
	MD	headpiece subdomain. Nature Structural Biology. 4(3), 180-184.
31	170	McKnight, C.J., et al. (1996). A Thermostable 35-Residue Subdomain within Villin Headpiece.
	MASS	Journal of Molecular Biology. 260, 126-134.
32	TWE T	Xu, D. and R. Nussinov. (1997). Favorable domain size in proteins. Folding & Design. 3, 11-17.
il	100	
33	1.0	Kippen, A.D. and AR. Fersht. (1995). Analysis of the Mechanism of Assembly of Cleaved Barnase
	IM	from Two Peptide Fragments and Its Relevance to the Folding Pathway of Uncleaved Barnase.
	1/1/27	Biochemistry. 34, 1464-1468.
34	10/20	Gay, G.d.P. and A.R. Fersht. (1994). Generation of a Family of Protein Fragments for Structure-
	MATA	Folding Studies. 1. Folding Complementation of Two Fragments of Chymotrypsin Inhibitor-2
	100	Formed by Cleavage at Its Unique Methionine Residue. Biochemistry. 33, 7957-7963.
35	Res	Wu, L.C., R. Grandori, and J. Carey. (1994). Autonomous subdomains in protein folding. Protein
L	1 1	Science

JUL 27 2001 JUL



		CURLINIED MARK
T TO	>	Science. 3, 369-371.
36	BADEN	1 22
1	DOX-	degradation rate and expression yield of barnase variants in the periplasm of Escherichia coli. Protein
	\$H2	Engineering. 9(12), 1197-1202.
37	820	Axe, D.D., N.W. Foster, and A.R. Fersht. (1996). Active barnase variants with completely random
	11/2	hydrophobic cores. Proc. Natl. Acad. Sci. USA. 93, 5590-5594.
38	ANZ	Waldburger, C.D., J.F. Schildbach, and R.T. Sauer. (1995). Are buried salt bridges important for protein
	MO)	stability and conformational specificity? Nature Structural Biology. 2(2), 122-128.
39	201	Roy, S., et al. (1997). A Protein Designed by Binary Patterning of Polar and Nonpolar Amino Acids
	1777	Displays Native-like Properties. Journal of the American Chemical Society. 119, 5302-5306.
40	N/C	Clackson, T., et al. (1991). Making antibody fragments using phage display libraries. Nature. 352, 624-
	#1	628
41	200	McCafferty, J., et al. (1990). Phage antibodies: filamentous phage displaying antibody variable
	1117	domains. <i>Nature</i> . 348 , 552-554.
42	3.00	Fisch, I., et at. (1996). A strategy of exon shuffling for making large peptide repertoires displayed on
	MIZ.	filamentous bacteriophage. Proc. Natl. Acad. Sci. USA. 93, 7761-7766.
43	1	Matouschek, A., et al. (1989). Mapping the transition state and pathway of protein folding by protein
	#47	engineering. Nature. 340, 122-126.
44	100	Laemmli, U.K. (1970). Cleavage of structural proteins during the assembly of the head of bacteriophage
	M	T4. Nature. 227, 680-685.
45	1800	Schatz, G. and Dobberstein, B. (1996). Common principles of protein translocation across
	THE WAY	membranes. Science. 271, 1519-1526.
46	NO	Von Heijne, G. (1998). Life and death of a signal peptide. Nature. 396, 111-113.
47	000	Sprengart, M.L., Fuchs, E. and Porter, A.G. (1996). The downstream box: an efficient and independent
	MIL	translation initiation signal in E.coli. The EMBO Journal. 15, 665-674.
48		Perlman, D. and Halvorson, H.O. (1983). A putative signal peptidase recognition site and sequence in
	1200	eukaryotic and prokaryotic signal peptides. Journal of Molecular Biology. 167, 391-409.
49	DAK	Von Heijne, G. (1983). Patterns of amino acids near signal-sequence cleavage sites. Eur. J. Biochem. 133,
	+45) 17-21.
50	No	Pedersen, H., Hölder, S., Sutherlin, D.P., Schwitter, U., King, D.S., Schultz, P.G. (1998). Proc. Natl.
	11	Acad. Sci. USA. 95, 10523-10528.
EXAL	mm /	DATE CONSIDERED
EXAM	IINEK (Maher # 2005
*EXAMIN	ER: Initial il refe	rence considered, whether or not citation is in conformance with MPEP 609. Draw line through citation if not in conformance and not considered. Include copy of this form with
next comm	unication to Appli	callt
**Copies o	of references not pr	ovided at the time of this submission.